REMARKS

Claim 57 has been canceled.

Claim 40 has been amended so that SEQ ID NO's 30 & 33 no longer appear in the language of the claim. In addition, the function of eliciting an immune response now refers to proteins having specific SEQ ID NO's as opposed to referring to "naturally occurring canine or feline B7-2 proteins." Support for such a function can be found in the specification, for example, on page 10, lines 7-28, page 26, lines 14-23, and page 30, lines 3-20. With regard to T-cell proliferation, the language has been altered so that T-cell proliferation now occurs in the presence of an antigen that binds T-cell receptor. Applicants believe this language adds clarity to the claims. Support for such language can be found in the specification, for example, on page 1, lines 9-17.

Claim 41 has been amended to remove language referring to naturally occurring B7-2 proteins. In addition, the claim now specifies nucleic acid molecules 95% identical to SEQ ID NO:33, nucleic acid molecules encoding a protein 95% identical to SEQ ID NO:34 and nucleic acid molecules comprising the sequence of SEQ ID NO:30. The Claim also now specifies the function of eliciting an immune response or stimulating T-cell proliferation. With regard to T-cell proliferation, the language has been altered so that T-cell proliferation now occurs in the presence of an antigen that binds T-cell receptor. Applicants believe this language adds clarity to the claims.

Claim 42 has been amended so that SEQ ID NO's 30 & 33 no longer appear in the language of the claim.

Claim 43 has been amended so that SEQ ID NO's 6, 9, 16, 19, 25 and 28 no longer appear in the language of the claim.

Claim 44 has been amended to include nucleic acid molecules complimentary to those already described by the claim. In addition, the function of eliciting an immune response now refers to proteins having specific SEQ ID NO's as opposed to referring to "naturally occurring canine or feline B7-2 proteins." With regard to T-cell proliferation, the language has been altered so that T-cell proliferation now occurs in the presence of an antigen that binds T-cell receptor. Applicants believe this language adds clarity to the claims.

Claim 45 has been amended so that SEQ ID NO's 31 & 34 no longer appear in the language of the claim.

Claim 46 has been amended so that it no longer refers to allelic variants. The claim now specifies the nucleic acid molecules encode proteins having the specified amino acid sequences.

Claim 47 has been re-drafted to clarify the language of the claim. In addition, reference to SEQ ID NO's 30 & 33 has been removed from the claim. Finally, the claim now also refers to nucleic acid molecules complementary to the already specified SEQ ID NO's.

Claim 50 has been amended to read "as specified in any one of" when referring to Claims 40-49.

Claim 51 has been amended so that SEQ ID NO's 30 & 33 no longer appear in the language of the claim. In addition, reference to naturally occurring B7-2 proteins has been removed from the claim. Finally, functional language, identical to that listed for example in Claim 40, has been added to the claim.

Claim 52 has been amended so that SEQ ID NO's 31 & 34 no longer appear in the language of the claim.

Claim 53, has been amended so that SEQ ID NO's 30 & 33 no longer appear in the language of the claim.

Claim 54 has been amended so that SEQ ID NO's 31 & 34 no longer appear in the language of the claim.

Claim 55 has been amended to remove reference to allelic variant sand naturally occurring B7-2 proteins. The claim now specifies a method to produce a protein using the nucleic acid molecule of Claim 41.

Claim 56 has been amended so that SEQ ID NO's 30 & 33 no longer appear in the language of the claim.

Claims 59-61 have been amended to correct improper multiple dependencies. Specifically, the Claims now refer to "any one of" Claims 40-49.

Claim Objections

With respect to the improper dependencies noted by the Examiner, Applicants note Claim 57 has been canceled. Additionally, Claims 46, 50, 55 and 59-61 have been amended to either remove or correct the multiple dependency language.

With respect to Claim 43, the wayward period has been dealt with and should no longer present a problem.

Rejections Under 35 U.S.C. §112, second paragraph

The Examiner has rejected Claim 43 for lack of antecedent basis for SEQ ID NO's encoding non-soluble B7-2 proteins, since Claim 41, from which Claim 43 depends, requires the nucleic acid molecules encode a soluble B7-2 protein. Applicants note Claim 41 has been amended to remove the requirement that the encoded proteins be soluble.

The Examiner has also rejected Claims 53, 54 and 55 for referring to the method of Claim 50, when in fact, Claim 50 is to composition. Applicants note the dependency in Claims 53-55 has been changed so these claims now depend from Claim 51 which specifies a method.

Rejections Under 35 U.S.C. §112 second paragraph

The Examiner has rejected Claims 40-46, 50-55 and 59-61 for lack of written description and lack of enablement. Specifically, the Examiner states some claims to nucleic acid molecules about 95% identical to reference molecules lack a functional description and therefore have not been adequately described or enabled. In addition, there is not adequate written description or enablement for allelic variants or "naturally occurring canine or feline B7-2 proteins."

Applicants note that functional language has been added to claims, in particular Claims 51-52, specifying nucleic acids about 95% identical to reference sequences. In addition, although Applicants believe the use of the term "allelic variant" is supported in the specification, all reference to allelic variants have been removed from the claim set. Likewise, although Applicants believe "naturally occurring canine and feline B7-2 proteins" are adequately described and enabled in the specification, in order to expedite prosecution, Applicants have replaced all such language in the claims with language that references a particular SEQ ID NO.

Rejections Under 35 U.S.C §§ 102 and 103

The Examiner has rejected Claims 40, 44, 46-52 and 55-61 as being anticipated by Collisson stating that Collisson is available as a reference as of May 1, 1998. Collisson teaches SEQ ID NO:5, a nucleic acid sequence encoding a feline B7-2 protein, that is 98% identical to the coding region of instant SEQ ID NO:28 and 95% identical to instant SEQ ID NO:26.

Applicants note that SEQ ID NO's 1-29 were disclosed on April 17, 1998, prior to Collissons filing date of May 1, 1998. It is only SEQ ID NO's 31-35 that were disclosed on March 19, 1999 which is after Collissons priority date. Applicants note that the Claims have been amended so that SEQ ID NO's 31-35 are not claimed in the same claim as SEQ ID NO's 1-

29. For example, Claim 40 now lists only SEQ ID NO's 6, 9, 16, 19, 25 and 28 and therefore should be accorded a priority date of April 17, 1998 which is earlier than Collissons priority date. With respect to SEQ ID NO's 30-35, Claim 41 claims nucleic acid sequences at least about 95% identical to SEQ ID NO:33 and amino acid sequences 95% identical to SEQ ID NO:34. Applicants note that Collisson cannot be considered prior art to these sequences for the following reasons.

There are two forms of the B7-2 protein, a full length form, which contains a transmembrane domain, and a soluble form lacking the transmembrane domain. The soluble form of the B7-2 protein is encoded by a nucleic acid molecule created by alternative splicing of the cDNA encoding the full-length form. SEQ ID NO:5 disclosed by Collisson is the sequence of the gene encoding the full-length form of the feline B7-2 protein. Instant SEQ ID NO:33 encodes the soluble form of the feline B7-2 protein and therefore lacks the sequences encoding the transmembrane domain which are present in SEQ ID NO:5. Collisson discloses no such sequence. As a result of its lacking the transmembrane domain coding region, SEQ ID NO:33 shares less than 95% identity with SEQ ID NO:5 of Collisson. Below is an alignment of SEQ ID NO:33 with the corresponding region of SEQ ID NO:5. This alignment demonstrates these two sequences share, at best, 69% identity:

align Results

Please site: *Pearson, W.R., Wood, T., Zhang, Z., and Miller, W. (1997) Comparison of DNA sequences with protein sequences, Genomics 46: 24-36*

```
>_ SIN5                                                    509 nt vs.
>_ SIN33                                                   359 nt
scoring matrix: , gap penalties: -12/-2
69.0% identity;          Global alignment score: 1056

               10         20         30         40         50         60
SIN05  ATACAAGGTTACCCAGAACCTAAGGAGATGTATTTTCAGCTAAACACTGAGAATTCAACT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SIN33  ATACAAGGTTACCCAGAACCTAAGGAGATGTATTTTCAGCTAAACACTGAGAATTCAACT
               10         20         30         40         50         60

               70         80         90        100        110        120
SIN05  ACTAAGTATGATACTGTCATGAAGAAATCTCAAAATAATGTGACAGAACTGTACAACGTT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SIN33  ACTAAGTATGATACTGTCATGAAGAAATCTCAAAATAATGTGACAGAACTGTACAACGTT
               70         80         90        100        110        120
```

```
            130       140       150       160       170       180
SIN05  TCTATCAGCTTGCCTTTTTCAGTCCCTGAAGCACACAATGTGAGCGTCTTTTGTGCCCTG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SIN33  TCTATCAGCTTGCCTTTTTCAGTCCCTGAAGCACACAATGTGAGCGTCTTTTGTGCCCTG
            130       140       150       160       170       180

            190       200       210       220       230       240
SIN05  AAACTGGAGACACTGGAGATGCTGCTCTCCCTACCTTTCAATATAGATGCACAACCTAAG
       ::::::::::::::::::::::::::::::::::::::::::::
SIN33  AAACTGGAGACACTGGAGATGCTGCTCTCCCTACCTTTCAATATAGA------------
            190       200       210       220

            250       260       270       280       290       300
SIN05  GATAAAGACCCTGAACAAGGCCACTTCCTCTGGATTGCGGCTGTACTTGTAATGTTTGTT

_      ------------------------------------------------------------


            310       320       330       340       350       360
SIN05  GTTTTTTGTGGGATGGTGTCCTTTAAAACACTAAGGAAAAGGAAGAAGAAGCAGCCTGGC

_      ------------------------------------------------------------


            370       380       390       400       410       420
SIN05  CCCTCTCATGAATGTGAAACCATCAAAAGGGAGAGAAAAGAGAGCAAACAGACCAACGAA
                     ::::::::::::::::::::::::::::::::::::::::::::
SIN33  -----------------AACCATCAAAAGGGAGAGAAAAGAGAGCAAACAGACCAACGAA
                     230       240       250       260       270

            430       440       450       460       470       480
SIN05  AGAGTACCATACCACGTACCTGAGAGATCTGATGAAGCCCAGTGTGTTAACATTTTGAAG
       :::::::::::::::::::::::::::::::::::::::::::: ::::::::::::::
SIN33  AGAGTACCATACCACGTACCTGAGAGATCTGATGAAGCCCAGTGTATTAACATTTTGAAG
            280       290       300       310       320       330

            490       500
SIN05  ACAGCCTCAGGGGACAAAAATCAGTAGG-A
       :::::::::: ::::::: : : ::   :
SIN33  ACAGCCTCAGGCGACAAAAGT-ACTACACA
            340       350
```

With respect to SEQ ID NO:30, Applicants note that Claim 41 now claims a nucleic acid sequence comprising the sequence of SEQ ID NO:30. Alignment of SEQ ID NO:30 with the corresponding region of Collissons SEQ ID NO:5 (shown below) demonstrates that these sequences are not 100% identical but, due sequence variation at their 3' ends, are instead 98.4% identical.

align Results

Please site: *Pearson, W.R., Wood, T., Zhang, Z., and Miller, W. (1997) Comparison of DNA sequences with protein sequences, Genomics 46: 24-36*

```
>_ SIN5                                                    509 nt vs.
>_ SIN30                                                   509 nt
scoring matrix: , gap penalties: -12/-2
98.4% identity;         Global alignment score: 1966

               10        20        30        40        50        60
SIN05  ATACAAGGTTACCCAGAACCTAAGGAGATGTATTTTCAGCTAAACACTGAGAATTCAACT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SIN30  ATACAAGGTTACCCAGAACCTAAGGAGATGTATTTTCAGCTAAACACTGAGAATTCAACT
               10        20        30        40        50        60

               70        80        90       100       110       120
SIN05  ACTAAGTATGATACTGTCATGAAGAAATCTCAAAATAATGTGACAGAACTGTACAACGTT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SIN30  ACTAAGTATGATACTGTCATGAAGAAATCTCAAAATAATGTGACAGAACTGTACAACGTT
               70        80        90       100       110       120

              130       140       150       160       170       180
SIN05  TCTATCAGCTTGCCTTTTTCAGTCCCTGAAGCACACAATGTGAGCGTCTTTTGTGCCCTG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SIN30  TCTATCAGCTTGCCTTTTTCAGTCCCTGAAGCACACAATGTGAGCGTCTTTTGTGCCCTG
              130       140       150       160       170       180

              190       200       210       220       230       240
SIN05  AAACTGGAGACACTGGAGATGCTGCTCTCCCTACCTTTCAATATAGATGCACAACCTAAG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SIN30  AAACTGGAGACACTGGAGATGCTGCTCTCCCTACCTTTCAATATAGATGCACAACCTAAG
              190       200       210       220       230       240

              250       260       270       280       290       300
SIN05  GATAAAGACCCTGAACAAGGCCACTTCCTCTGGATTGCGGCTGTACTTGTAATGTTTGTT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SIN30  GATAAAGACCCTGAACAAGGCCACTTCCTCTGGATTGCGGCTGTACTTGTAATGTTTGTT
              250       260       270       280       290       300

              310       320       330       340       350       360
SIN05  GTTTTTTGTGGGATGGTGTCCTTTAAAACACTAAGGAAAAGGAAGAAGAAGCAGCCTGGC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SIN30  GTTTTTTGTGGGATGGTGTCCTTTAAAACACTAAGGAAAAGGAAGAAGAAGCAGCCTGGC
              310       320       330       340       350       360

              370       380       390       400       410       420
SIN05  CCCTCTCATGAATGTGAAACCATCAAAAGGGAGAGAAAAGAGAGCAAACAGACCAACGAA
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SIN30  CCCTCTCATGAATGTGAAACCATCAAAAGGGAGAGAAAAGAGAGCAAACAGACCAACGAA
              370       380       390       400       410       420

              430       440       450       460       470       480
SIN05  AGAGTACCATACCACGTACCTGAGAGATCTGATGAAGCCCAGTGTGTTAACATTTTGAAG
       :::::::::::::::::::::::::::::::::::::::::::: ::::::::::::::
SIN30  AGAGTACCATACCACGTACCTGAGAGATCTGATGAAGCCCAGTGTATTAACATTTTGAAG
              430       440       450       460       470       480
```

```
              490        500
SIN05  ACAGCCTCAGGGGACAAAAATCAGTAGG-A
       :::::::::::: ::::::: : : ::    :
SIN30  ACAGCCTCAGGCGACAAAAGT-ACTACACA
              490        500
```

Similar result (97.6% identity) are seen if the corresponding protein sequences (SEQ ID NO:6 and SEQ ID NO:31) are aligned.

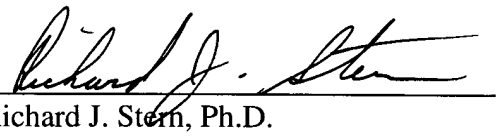
Based on the alignments shown above, Applicants believe that Collisson cannot be considered prior art for the current claims set.

CONCLUSION

In light of the amendments and remarks above, Applicants request the withdrawal of all rejections and solicit an allowance of the newly submitted claims. The Examiner is invited to contact the undersigned should any issues remain.

Respectfully submitted,

Dated: September 18, 2003

By: 

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